

## SEQUENCE LISTING

<110> Tsuchiya, Masayuki  
Saito, Mikiyoshi  
Ohtomo, Toshihiko

<120> NOVEL METHOD FOR GENE CLONING

<130> 06501-070001

<140> US 09/700,820

<141> 2000-11-20

<150> PCT/JP99/02341

<151> 1999-04-30

<150> JP 10/138652

<151> 1998-05-20

<150> JP 10/279876

<151> 1998-10-01

<160> 39

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Peptide Linker Sequence

<400> 1

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

<210> 2

<211> 1035

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1035)

<400> 2

atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg 48  
Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro  
1 5 10 15

gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga 96  
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg  
20 25 30

ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg 144  
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro  
35 40 45

ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys 50 55 60	192
ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg 65 70 75 80	240
ctg ctg ctg agg tcg gtg cag ctc cac gac tct gga aac tat tca tgc Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys 85 90 95	288
tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val 100 105 110	336
ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser 115 120 125	384
aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr 130 135 140	432
aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp 145 150 155 160	480
ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys 165 170 175	528
cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met 180 185 190	576
tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe 195 200 205	624
cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val 210 215 220	672
act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp 225 230 235 240	720
ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg 245 250 255	768
tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp 260 265 270	816

ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac 864  
 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His  
           275                          280                          285

gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc 912  
 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser  
           290                          295                          300

gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt 960  
 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser  
           305                          310                          315                          320

cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act 1008  
 Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr  
                                   325                                  330                                  335

aat aaa gac gat gat aat att ctc ttc 1035  
 Asn Lys Asp Asp Asp Asn Ile Leu Phe  
                           340                          345

<210> 3  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "IL6R1", an artificially synthesized primer sequence

<400> 3  
 ttccaattcc caccatgctg gccgtcggct gcgcgctgct 40

<210> 4  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "IL6R2", an artificially synthesized primer sequence

<400> 4  
 ttccaattcg aagagaatat tatcatcgtc tttatt 36

<210> 5  
 <211> 768  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(768)

<220>  
 <223> Description of Artificial Sequence: a designed single chain Fv gene sequence

<400> 5

cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln	
1 5 10 15	
acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat	96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp	
20 25 30	
cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg	144
His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp	
35 40 45	
att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc	192
Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu	
50 55 60	
aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc	240
Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser	
65 70 75 80	
ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt	288
Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc	336
Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly	
100 105 110	
agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt	384
Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
115 120 125	
tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc cca agc agc	432
Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
130 135 140	
ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc	480
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
145 150 155 160	
cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag	528
Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
165 170 175	
gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac tct ggt gtg	576
Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
180 185 190	
cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc	624
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
195 200 205	
atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag	672
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
210 215 220	

ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc 720  
 Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 225 230 235 240

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat 768  
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 245 250 255

<210> 6  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "TMT1", an artificially synthesized primer sequence

<400> 6  
 ggtgtcgcact ccaggtcca actgcaggag ag 32

<210> 7  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "LINK1", an artificially synthesized primer sequence

<400> 7  
 ctgcgtcacag tctctcagg tgggtggtggt tc 32

<210> 8  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "LINK3", an artificially synthesized primer sequence

<400> 8  
 gacatccaga tgaccagag cccaagcagc ctgagcgc 38

<210> 9  
 <211> 63  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "SCP-C", an artificially synthesized primer sequence

<400> 9  
 gctgaattct tattatttat cgtcatcgtc tttgtagtca agcttatcag atggcgggaa 60

gat 63

<210> 10  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: FLAG peptide

<400> 10  
 Met Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 11  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "LINK2", an artificially synthesized primer sequence

<400> 11  
 aaccaccacc acctgaggag actgtgacga ggct 34

<210> 12  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "LINK4", an artificially synthesized primer sequence

<400> 12  
 aggctgcttg ggctctgggt catctggatg tccga 35

<210> 13  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "TMT2", an artificially synthesized primer sequence

<400> 13  
 atccgcggcc gcttattatt tatcgtcacg gtcttt 36

<210> 14  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: leader sequence  
 <400> 14

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15

Val Asp Ser

<210> 15  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "S-FLAG1", an artificially synthesized oligonucleotide sequence

<400> 15  
 aattcccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60  
 cgactccgac tacaagacg atgacgataa aggtaccgcg gccgcg 106

<210> 16  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "S-FLAG2", an artificially synthesized oligonucleotide sequence

<400> 16  
 gatccgcggc cgcggtacct ttatcgtcat cgtctttgta gtcggagtcg acacctgtag 60  
 ctgttgctac caagaagagg atgatacagc tccatcccat ggtggg 106

<210> 17  
 <211> 2995  
 <212> DNA  
 <213> Mus musculus

<220>

<221> CDS

<222> (29)..(2839)

<400> 17  
 gaattccgga catctagagg cagcgaactt gtttccgatt catgctttat catttcttaa 60  
 ttctgtatgt tgggaacatc cctgcaag atg tca gca cca agg att tgg cta 112  
 Met Ser Ala Pro Arg Ile Trp Leu  
 1 5

gcg caa gct ttg ctt ttt ttc ctc acc act gaa tct ata ggt caa ctt 160  
 Ala Gln Ala Leu Leu Phe Phe Leu Thr Thr Glu Ser Ile Gly Gln Leu  
 10 15 20

ttg gaa ccg tgt ggt tac atc tac cct gaa ttt cca gtt gtc cag cgc 208  
 Leu Glu Pro Cys Gly Tyr Ile Tyr Pro Glu Phe Pro Val Val Gln Arg  
 25 30 35 40

ggc tgc aac ttc act gcc att tgt gtg ctg aag gag gcg tgt ctg cag	256
Gly Ser Asn Phe Thr Ala Ile Cys Val Leu Lys Glu Ala Cys Leu Gln	
45 50 55	
cat tac tac gtg aat gcc agc tac atc gtg tgg aag acc aac cat gct	304
His Tyr Tyr Val Asn Ala Ser Tyr Ile Val Trp Lys Thr Asn His Ala	
60 65 70	
gct gtt ccc agg gag cag gtc act gtc atc aac aga acc acg tcc agt	352
Ala Val Pro Arg Glu Gln Val Thr Val Ile Asn Arg Thr Thr Ser Ser	
75 80 85	
gtc acg ttc aca gac gtg gtc ctc ccg agc gtg cag ctc acc tgc aac	400
Val Thr Phe Thr Asp Val Val Leu Pro Ser Val Gln Leu Thr Cys Asn	
90 95 100	
atc ctg tcc ttt ggg cag atc gag cag aat gtg tat gga gtc acc atg	448
Ile Leu Ser Phe Gly Gln Ile Glu Gln Asn Val Tyr Gly Val Thr Met	
105 110 115 120	
ctt tca ggc ttt cct cca gat aaa cct aca aat ttg act tgc att gtg	496
Leu Ser Gly Phe Pro Pro Asp Lys Pro Thr Asn Leu Thr Cys Ile Val	
125 130 135	
aat gag ggg aag aat atg ctg tgc cag tgg gac ccc gga agg gag act	544
Asn Glu Gly Lys Asn Met Leu Cys Gln Trp Asp Pro Gly Arg Glu Thr	
140 145 150	
tac ctt gaa aca aac tac act ttg aaa tca gag tgg gca aca gag aag	592
Tyr Leu Glu Thr Asn Tyr Thr Leu Lys Ser Glu Trp Ala Thr Glu Lys	
155 160 165	
ttt cct gat tgc cag tca aag cat ggc act tca tgt atg gtc agc tac	640
Phe Pro Asp Cys Gln Ser Lys His Gly Thr Ser Cys Met Val Ser Tyr	
170 175 180	
atg ccc acc tat tat gtc aac att gaa gtc tgg gtg gaa gca gag aat	688
Met Pro Thr Tyr Tyr Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn	
185 190 195 200	
gcc ctt ggg aag gtc tcc tca gag tct atc aat ttt gac ccc gtg gat	736
Ala Leu Gly Lys Val Ser Ser Glu Ser Ile Asn Phe Asp Pro Val Asp	
205 210 215	
aaa gtg aaa ccc acc cca cca tat aat tta tca gtg acc aac tca gaa	784
Lys Val Lys Pro Thr Pro Pro Tyr Asn Leu Ser Val Thr Asn Ser Glu	
220 225 230	
gaa tta tcc agt ata tta aag cta tca tgg gtc agt tca ggg ctg ggc	832
Glu Leu Ser Ser Ile Leu Lys Leu Ser Trp Val Ser Ser Gly Leu Gly	
235 240 245	
ggt ctt tta gat cta aag tct gac atc caa tat agg acc aaa gat gcc	880
Gly Leu Leu Asp Leu Lys Ser Asp Ile Gln Tyr Arg Thr Lys Asp Ala	
250 255 260	



tca act tgg atc cag gtc cct ctt gaa gat aca atg tct cct cga act	928
Ser Thr Trp Ile Gln Val Pro Leu Glu Asp Thr Met Ser Pro Arg Thr	
265 270 275 280	
tcc ttc act gtg cag gac ctc aag cct ttt aca gaa tat gtg ttt agg	976
Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg	
285 290 295	
atc cgg tcc att aag gac agt ggg aag ggc tac tgg agt gac tgg agt	1024
Ile Arg Ser Ile Lys Asp Ser Gly Lys Gly Tyr Trp Ser Asp Trp Ser	
300 305 310	
gag gag gct agt ggg acc aca tac gaa gac aga cca tcc aga cca cca	1072
Glu Glu Ala Ser Gly Thr Thr Tyr Glu Asp Arg Pro Ser Arg Pro Pro	
315 320 325	
agt ttc tgg tat aag aca aat cca tcc cat ggg cag gaa tat aga tct	1120
Ser Phe Trp Tyr Lys Thr Asn Pro Ser His Gly Gln Glu Tyr Arg Ser	
330 335 340	
gta cgg ctc ata tgg aag gca ctg cct ctt tct gaa gcc aat ggg aaa	1168
Val Arg Leu Ile Trp Lys Ala Leu Pro Leu Ser Glu Ala Asn Gly Lys	
345 350 355 360	
atc ttg gat tat gaa gtg att ctt acg cag tca aag tcc gtc tca caa	1216
Ile Leu Asp Tyr Glu Val Ile Leu Thr Gln Ser Lys Ser Val Ser Gln	
365 370 375	
acg tac aca gtc act ggc aca gag ctg acc gtg aat ctc acc aat gac	1264
Thr Tyr Thr Val Thr Gly Thr Glu Leu Thr Val Asn Leu Thr Asn Asp	
380 385 390	
cgc tat gtc gcg tct cta gca gca aga aac aag gtg ggc aaa tca gct	1312
Arg Tyr Val Ala Ser Leu Ala Ala Arg Asn Lys Val Gly Lys Ser Ala	
395 400 405	
gca gct gtc ctc acc atc ccc agc ccc cac gtc aca gct gct tat tct	1360
Ala Ala Val Leu Thr Ile Pro Ser Pro His Val Thr Ala Ala Tyr Ser	
410 415 420	
gta gtg aat ctt aaa gca ttt cca aaa gat aac ctg ctc tgg gtg gaa	1408
Val Val Asn Leu Lys Ala Phe Pro Lys Asp Asn Leu Leu Trp Val Glu	
425 430 435 440	
tgg aca cct cca cct aaa ccc gtg agc aag tac atc tta gag tgg tgt	1456
Trp Thr Pro Pro Pro Lys Pro Val Ser Lys Tyr Ile Leu Glu Trp Cys	
445 450 455	
gtg ttg tca gag aac gca ccc tgt gtt gaa gac tgg cag cag gaa gac	1504
Val Leu Ser Glu Asn Ala Pro Cys Val Glu Asp Trp Gln Gln Glu Asp	
460 465 470	
gct acc gtg aat cgg acc cac ttg aga gga cgc ctc ctg gag agc aag	1552
Ala Thr Val Asn Arg Thr His Leu Arg Gly Arg Leu Leu Glu Ser Lys	
475 480 485	
tgc tat caa atc aca gta act ccc gta ttc gcc acg ggg ccc gga ggc	1600

Cys 490	Tyr	Gln	Ile	Thr	Val	Thr 495	Pro	Val	Phe	Ala	Thr 500	Gly	Pro	Gly	Gly	
tct	gag	tcc	ttg	aag	gcg	tac	ctc	aaa	caa	gcc	gct	cct	gcc	aga	gga	1648
Ser 505	Glu	Ser	Leu	Lys	Ala 510	Tyr	Leu	Lys	Gln	Ala 515	Ala	Pro	Ala	Arg	Gly 520	
ccg	act	gtt	cgg	aca	aag	aaa	gtg	ggg	aaa	aat	gaa	gct	gtc	tta	gcg	1696
Pro	Thr	Val	Arg	Thr 525	Lys	Lys	Val	Gly	Lys 530	Asn	Glu	Ala	Val	Leu	Ala 535	
tgg	gac	cag	att	cct	gtg	gac	gac	cag	aat	ggc	ttc	att	aga	aac	tac	1744
Trp	Asp	Gln	Ile 540	Pro	Val	Asp	Asp	Gln 545	Asn	Gly	Phe	Ile 550	Arg	Asn	Tyr	
tcc	ata	tct	tac	aga	acc	agc	gtg	gga	aag	gag	atg	gtt	gtg	cat	gtg	1792
Ser	Ile 555	Ser	Tyr	Arg	Thr	Ser	Val 560	Gly	Lys	Glu	Met 565	Val	Val	His	Val	
gat	tct	tct	cac	acg	gag	tac	acg	ctg	tcc	tct	ctg	agt	agt	gat	acg	1840
Asp	Ser	Ser	His	Thr	Glu	Tyr 575	Thr	Leu	Ser	Ser 580	Leu	Ser	Ser	Asp	Thr	
ttg	tac	atg	gtc	cga	atg	gcc	gcg	tac	aca	gat	gaa	ggg	ggg	aaa	gat	1888
Leu 585	Tyr	Met	Val	Arg	Met 590	Ala	Ala	Tyr	Thr	Asp 595	Glu	Gly	Gly	Lys	Asp 600	
ggg	ccg	gaa	ttc	act	ttt	aca	aca	cca	aag	ttc	gct	caa	gga	gaa	ata	1936
Gly	Pro	Glu	Phe	Thr 605	Phe	Thr	Thr	Pro	Lys 610	Phe	Ala	Gln	Gly	Glu	Ile 615	
gaa	gcc	ata	gtc	gtg	cct	gtg	tgc	tta	gcc	ttc	ctc	ctg	aca	acc	ctg	1984
Glu	Ala	Ile	Val 620	Val	Pro	Val	Cys	Leu	Ala 625	Phe	Leu	Leu	Thr	Thr	Leu 630	
ctg	ggc	gtc	ttg	ttc	tgc	ttt	aac	aaa	cga	gac	cta	att	aaa	aaa	cac	2032
Leu	Gly 635	Val	Leu	Phe	Cys	Phe 640	Asn	Lys	Arg	Asp	Leu 645	Ile	Lys	Lys	His	
atc	tgg	cct	aat	gtt	cct	gat	cct	tcc	aag	agt	cat	att	gcc	cag	tgg	2080
Ile	Trp 650	Pro	Asn	Val	Pro	Asp 655	Pro	Ser	Lys	Ser 660	His	Ile	Ala	Gln	Trp	
tca	cct	cac	acc	ccc	cca	agg	cac	aat	ttt	aac	tcc	aaa	gat	caa	atg	2128
Ser 665	Pro	His	Thr	Pro	Pro 670	Arg	His	Asn	Phe	Asn 675	Ser	Lys	Asp	Gln	Met 680	
tac	tcg	gac	ggc	aat	ttc	act	gat	gta	agc	gtt	gtg	gaa	ata	gaa	gca	2176
Tyr	Ser	Asp	Gly	Asn 685	Phe	Thr	Asp	Val	Ser 690	Val	Val	Glu	Ile	Glu	Ala 695	
aac	aac	aag	aag	cct	tgt	cca	gat	gac	ctg	aag	tcc	gtg	gac	ctg	ttc	2224
Asn	Asn	Lys	Lys	Pro	Cys	Pro	Asp	Asp	Leu 705	Lys	Ser	Val	Asp	Leu	Phe 710	
aag	aag	gag	aaa	gtg	agt	aca	gaa	ggg	cac	agc	agt	ggc	atc	ggg	ggc	2272
Lys	Lys	Glu	Lys	Val	Ser	Thr	Glu	Gly	His	Ser	Ser	Gly	Ile	Gly	Gly	

715	720	725	
tct tca tgc atg tcc tcc tcc agg ccc agc atc tcc agc aac gag gag Ser Ser Cys Met Ser Ser Ser Arg Pro Ser Ile Ser Ser Asn Glu Glu 730 735 740			2320
aat gag tct gct cag agc acc gcc agc acg gtc gag tac tcc act gtg Asn Glu Ser Ala Gln Ser Thr Ala Ser Thr Val Glu Tyr Ser Thr Val 745 750 755 760			2368
gtg cac agc ggc tac agg cac cag gtc ccg tcc gtg caa gtg ttc tca Val His Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser 765 770 775			2416
agg tcc gag tcc acc cag ccc ctg cta gac tcg gag gag cgg cca gaa Arg Ser Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu 780 785 790			2464
gac ctg cag ctg gtg gat agt gta gac ggt ggg gat gag atc ttg ccc Asp Leu Gln Leu Val Asp Ser Val Asp Gly Gly Asp Glu Ile Leu Pro 795 800 805			2512
agg caa ccg tat ttc aag cag aac tgc agt cag cct gaa gcc tgt cca Arg Gln Pro Tyr Phe Lys Gln Asn Cys Ser Gln Pro Glu Ala Cys Pro 810 815 820			2560
gag att tca cat ttt gaa agg tca aac cag gtt ttg tcc ggc aat gag Glu Ile Ser His Phe Glu Arg Ser Asn Gln Val Leu Ser Gly Asn Glu 825 830 835 840			2608
gag gat ttt gtc aga ctg aag cag cag cag gtt tca gat cac att tct Glu Asp Phe Val Arg Leu Lys Gln Gln Gln Val Ser Asp His Ile Ser 845 850 855			2656
cag ccc tat gga tcc gag caa cgg agg ctg ttt cag gaa ggc tct aca Gln Pro Tyr Gly Ser Glu Gln Arg Arg Leu Phe Gln Glu Gly Ser Thr 860 865 870			2704
gcg gat gct ctt ggc acg ggg gct gat gga cag atg gag aga ttt gaa Ala Asp Ala Leu Gly Thr Gly Ala Asp Gly Gln Met Glu Arg Phe Glu 875 880 885			2752
tct gtt gga atg gag acc aca att gat gaa gaa att ccc aaa agt tac Ser Val Gly Met Glu Thr Thr Ile Asp Glu Glu Ile Pro Lys Ser Tyr 890 895 900			2800
ttg cca cag act gta aga caa ggt ggc tac atg ccg cag tgaaggactg Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln 905 910 915			2849
gctcctgaac ttcagcagga actgcaaaat aaagctaaag acgagtggct tcagatgaga			2909
aacagtcctc actccctgaa gataggcatt gcctctaagg acaaagtcac acctgggccg			2969
tctccattcc agagtagctg gaattc			2995

<211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp1", an artificially synthesized primer sequence

<400> 18  
 cccaagcttg aattcacttt tacaaca

27

<210> 19  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp3", an artificially synthesized primer sequence

<400> 19  
 tttgcggccg cgaattccag ctactctgg

29

<210> 20  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "mgp2", an artificially synthesized primer sequence

<400> 20  
 cccaagcttg aattcaaaaa acacatctgg ctt

33

<210> 21  
 <211> 1662  
 <212> DNA  
 <213> Artificial Sequence

<220>

<221> CDS

<222> (11)..(1648)

<220>

<223> Description of Artificial Sequence: "hPM1-BvGS3 ", a designed single chain Fv gene sequence

<400> 21  
 gaattccacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca 49  
           Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr  
           1                  5                  10

gct aca ggt gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt 97  
 Ala Thr Gly Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
       15                  20                  25

ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	145
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
30 35 40 45	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	193
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
50 55 60	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	241
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
65 70 75	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	289
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
80 85 90	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	337
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
95 100 105	
acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	385
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
110 115 120 125	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	433
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
130 135 140	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg	481
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met	
145 150 155	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	529
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
160 165 170	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	577
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
175 180 185	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	625
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
190 195 200 205	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	673
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
210 215 220	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	721
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
225 230 235	
acc tac tac tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa	769
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
240 245 250	
ggg acc aag gtg gaa atc aaa tct aga ggt ggt ggt ggt tcg ggt ggt	817

Gly Thr Lys Val Glu Ile Lys Ser Arg Gly Gly Gly Gly Ser Gly Gly	
255 260 265	
ggg ggt tgc ggt ggt ggc gga tgc gtc gac tcc cag gtc caa ctg cag	865
Gly Gly Ser Gly Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln	
270 275 280 285	
gag agc ggt cca ggt ctt gtg aga cct agc cag acc ctg agc ctg acc	913
Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr	
290 295 300	
tgc acc gtg tct ggc tac tca att acc agc gat cat gcc tgg agc tgg	961
Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp	
305 310 315	
gtt cgc cag cca cct gga cga ggt ctt gag tgg att gga tac att agt	1009
Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser	
320 325 330	
tat agt gga atc aca acc tat aat cca tct ctc aaa tcc aga gtg aca	1057
Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr	
335 340 345	
atg ctg aga gac acc agc aag aac cag ttc agc ctg aga ctc agc agc	1105
Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser	
350 355 360 365	
gtg aca gcc gcc gac acc gcg gtt tat tat tgt gca aga tcc cta gct	1153
Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala	
370 375 380	
cgg act acg gct atg gac tac tgg ggt caa ggc agc ctc gtc aca gtc	1201
Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val	
385 390 395	
tcc tca ggt ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt ggc gga	1249
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
400 405 410	
tgc gac atc cag atg acc cag agc cca agc agc ctg agc gcc agc gtg	1297
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val	
415 420 425	
ggg gac aga gtg acc atc acc tgt aga gcc agc cag gac atc agc agt	1345
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser	
430 435 440 445	
tac ctg aat tgg tac cag cag aag cca gga aag gct cca aag ctg ctg	1393
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu	
450 455 460	
atc tac tac acc tcc aga ctg cac tct ggt gtg cca agc aga ttc agc	1441
Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser	
465 470 475	
ggg agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag	1489
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln	

480	485	490	
cca gag gac atc gct acc tac tac tgc caa cag ggt aac acg ctt cca			1537
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro			
495	500	505	
tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct			1585
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala			
510	515	520	525
gca cca tct gtc ttc atc ttc ccg cca tct gat aag ctt gac tac aaa			1633
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Lys Leu Asp Tyr Lys			
	530	535	540
gac gat gac gat aaa taataagcgg ccgc			1662
Asp Asp Asp Asp Lys			
	545		

&lt;210&gt; 22

&lt;211&gt; 72

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: "BvGS3", an artificially synthesized primer sequence

&lt;400&gt; 22

ggagtcgacc gatccgccac caccogaacc accaccaccc gaaccaccac cacctttgat 60

ttccaccttg gt

72

&lt;210&gt; 23

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(780)

&lt;220&gt;

<223> Description of Artificial Sequence: "shPM1( $\Delta$ EL)", a designed single chain Fv gene sequence

&lt;400&gt; 23

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1

5

10

15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96

Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg

20

25

30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile

35

40

45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggg caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggg ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa	780
Val Glu Ile Lys	
260	



```
<210> 24
<211> 321
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1) .. (321)
```

<400> 24																
cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	48
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	
1				5				10						15		
cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	96
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	
			20					25					30			
tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	144
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	
		35					40					45				
tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	192
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	
	50					55					60					
acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	240
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	
65					70					75					80	
aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	288
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	
				85				90						95		
ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tct						321
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Ser						
			100					105								

```
<210> 25
<211> 363
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (1) .. (363)
```

<400> 25																
gtg	gcc	ctg	cac	agg	ccc	gat	gtc	tac	ttg	ctg	cca	cca	gcc	cgg	gag	48
Val	Ala	Leu	His	Arg	Pro	Asp	Val	Tyr	Leu	Leu	Pro	Pro	Ala	Arg	Glu	
1				5					10					15		
cag	ctg	aac	ctg	cgg	gag	tcg	gcc	acc	atc	acg	tgc	ctg	gtg	acg	ggc	96
Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Ile	Thr	Cys	Leu	Val	Thr	Gly	
			20					25					30			

```

ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc 144
Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro
      35              40              45

```

```

ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag 192
Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln
      50              55              60

```

```

gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag 240
Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu
      65              70              75              80

```

```

gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc cat gag gcc ctg 288
Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala His Glu Ala Leu
      85              90              95

```

```

ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc gag ggg gag 336
Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Glu Gly Glu
      100              105              110

```

```

gtg agc gcc gac gag gag ggc ttt gag 363
Val Ser Ala Asp Glu Glu Gly Phe Glu
      115              120

```

<210> 26

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1101)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa", a designed single chain Fv gene sequence

<400> 26

```

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
      1              5              10              15

```

```

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
      20              25              30

```

```

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
      35              40              45

```

```

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly
      50              55              60

```

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggg caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgc ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggg ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	816
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
260 265 270	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	864
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
275 280 285	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	912

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
 290 295 300

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 960  
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 305 310 315 320

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 1008  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
 325 330 335

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 1056  
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
 340 345 350

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tct 1101  
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser  
 355 360 365

<210> 27

<211> 1143

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1143)

<220>

<223> Description of Artificial Sequence: "shPM1-MCH4", a designed single chain Fv gene sequence

<400> 27

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96  
 Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg  
 20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144  
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile  
 35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192  
 Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly  
 50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240  
 Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn  
 65 70 75 80

cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac 288  
 Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn

85																90				95				
cag	ttc	agc	ctg	aga	ctc	agc	agc	gtg	aca	gcc	gcc	gac	acc	gcg	gtt	336								
Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val									
100								105				110												
tat	tat	tgt	gca	aga	tcc	cta	gct	cgg	act	acg	gct	atg	gac	tac	tgg	384								
Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Ala	Arg	Thr	Thr	Ala	Met	Asp	Tyr	Trp									
115								120				125												
ggc	caa	ggc	agc	ctc	gtc	aca	gtc	tcc	tca	ggc	ggc	ggc	ggc	tcg	ggc	432								
Gly	Gln	Gly	Ser	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly									
130								135				140												
ggc	ggc	ggc	tcg	ggc	ggc	ggc	gga	tcg	gac	atc	cag	atg	acc	cag	agc	480								
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser									
145								150				155				160								
cca	agc	agc	ctg	agc	gcc	agc	gtg	ggc	gac	aga	gtg	acc	atc	acc	tgt	528								
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys									
				165								170				175								
aga	gcc	agc	cag	gac	atc	agc	agt	tac	ctg	aat	tgg	tac	cag	cag	aag	576								
Arg	Ala	Ser	Gln	Asp	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys									
				180								185				190								
cca	gga	aag	gct	cca	aag	ctg	ctg	atc	tac	tac	acc	tcc	aga	ctg	cac	624								
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His									
				195				200				205												
tct	ggc	gtg	cca	agc	aga	ttc	agc	ggc	agc	ggc	agc	ggc	acc	gac	ttc	672								
Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe									
210								215				220												
acc	ttc	acc	atc	agc	agc	ctc	cag	cca	gag	gac	atc	gct	acc	tac	tac	720								
Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr									
225								230				235				240								
tgc	caa	cag	gga	aat	act	tta	cca	tac	acg	ttc	ggc	caa	ggg	acc	aag	768								
Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys									
				245								250				255								
gtg	gaa	atc	aaa	gtg	gcc	ctg	cac	agg	ccc	gat	gtc	tac	ttg	ctg	cca	816								
Val	Glu	Ile	Lys	Val	Ala	Leu	His	Arg	Pro	Asp	Val	Tyr	Leu	Leu	Pro									
				260				265				270												
cca	gcc	cgg	gag	cag	ctg	aac	ctg	cgg	gag	tcg	gcc	acc	atc	acg	tgc	864								
Pro	Ala	Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Ile	Thr	Cys									
				275				280				285												
ctg	gtg	acg	ggc	ttc	tct	ccc	gcg	gac	gtc	ttc	gtg	cag	tgg	atg	cag	912								
Leu	Val	Thr	Gly	Phe	Ser	Pro	Ala	Asp	Val	Phe	Val	Gln	Trp	Met	Gln									
290								295				300												
agg	ggg	cag	ccc	ttg	tcc	ccg	gag	aag	tat	gtg	acc	agc	gcc	cca	atg	960								
Arg	Gly	Gln	Pro	Leu	Ser	Pro	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met									
305								310				315				320								

cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc 1008  
 Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr  
                   325                                  330                                  335

gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc 1056  
 Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala  
                   340                                  345                                  350

cat gag gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc 1104  
 His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser  
                   355                                  360                                  365

acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag 1143  
 Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu  
                   370                                  375                                  380

<210> 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "EF-1", an artificially synthesized primer sequence

<400> 28

cagacagtgg ttcaaagt

18

<210> 29

<211> 107

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-C2", an artificially synthesized primer sequence

<400> 29

aaagcggccg cttattatatt atcgtcacg tctttgtagt ctgaagcttt gatttccacc 60

ttggtcctt gcccgaaagt gtatggtaaa gtatttcctt gttggca

107

<210> 30

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1557)

<220>

<223> Description of Artificial Sequence: "shPM1( $\Delta$ EL)-BvGS3", a designed single chain Fv gene sequence

<400> 30

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	

tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa ggt ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt	816
Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
260 265 270	
ggc gga tgc gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	864
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	
275 280 285	
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	912
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
290 295 300	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	960
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
305 310 315 320	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	1008
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
325 330 335	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	1056
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
340 345 350	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	1104
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
355 360 365	
acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
370 375 380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
385 390 395 400	
ggt tgc ggt ggt ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg	1248
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met	
405 410 415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
420 425 430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344



Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr  
 435 440 445

cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc 1392  
 Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser  
 450 455 460

aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt 1440  
 Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
 465 470 475 480

acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct 1488  
 Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala  
 485 490 495

acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa 1536  
 Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln  
 500 505 510

ggg acc aag gtg gaa atc aaa 1557  
 Gly Thr Lys Val Glu Ile Lys  
 515

<210> 31

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappal", an artificially synthesized primer sequence

<400> 31

ccgccatctg atgagcagtt gaaatctgg 29

<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappa2", an artificially synthesized primer sequence

<400> 32

ttatttatcg tcatcgctctt tgtagtcaag cttagactct cccctgttga agct 54

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-K", an artificially synthesized primer sequence

<400> 33

ttcaactgct catcagatgg cgggaagat

29

<210> 34

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1878)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa-BvGS3", a designed single chain Fv gene sequence

<400> 34

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96  
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg  
20 25 30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144  
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile  
35 40 45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192  
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly  
50 55 60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240  
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn  
65 70 75 80

cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac 288  
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn  
85 90 95

cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt 336  
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
100 105 110

tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg 384  
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp  
115 120 125

ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgc ggt 432  
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
130 135 140

ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt	816
Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
260 265 270	
ggc gga tcg gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	864
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	
275 280 285	
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	912
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
290 295 300	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	960
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
305 310 315 320	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	1008
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
325 330 335	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	1056
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
340 345 350	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	1104
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
355 360 365	

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
370 375 380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
385 390 395 400	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg	1248
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met	
405 410 415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
420 425 430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
435 440 445	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	1392
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
450 455 460	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	1440
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
465 470 475 480	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	1488
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
485 490 495	
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa	1536
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
500 505 510	
ggg acc aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc	1584
Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe	
515 520 525	
atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt	1632
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val	
530 535 540	
gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg	1680
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp	
545 550 555 560	
aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca	1728
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr	
565 570 575	
gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg	1776
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr	
580 585 590	
ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc	1824

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
 595 600 605

acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga 1872  
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
 610 615 620

gag tct 1878  
 Glu Ser  
 625

<210> 35  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "MCH4-1", an artificially synthesized primer sequence

<400> 35  
 gtggaaatca aagtggccct gcacaggcc 29

<210> 36  
 <211> 68  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "MCH4-2.1", an artificially synthesized primer sequence

<400> 36  
 tagtcaagct tctcaaattc ctcttcgtcg gcgctaacct ctccttcggt ggacttgctc 60  
 acggtcct 68

<210> 37  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "SCP-Mu", an artificially synthesized primer sequence

<400> 37  
 tgcagggcca ctttgatttc caccttggt 29

<210> 38  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: "MCH4-2.2", an artificially synthesized primer sequence

&lt;400&gt; 38

aaagcggccg cttattattt atcgtcatcg tctttgtagt caagcttctc aaa 53

&lt;210&gt; 39

&lt;211&gt; 1920

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1920)

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: "shPM1-MCH4-BvGS3", a designed single chain Fv gene sequence

&lt;400&gt; 39

atg	gga	tgg	agc	tgt	atc	atc	ctc	ttc	ttg	gta	gca	aca	gct	aca	ggg	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1				5					10					15		

gtc	gac	tcc	cag	gtc	caa	ctg	cag	gag	agc	ggg	cca	ggg	ctt	gtg	aga	96
Val	Asp	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Arg	
			20					25					30			

cct	agc	cag	acc	ctg	agc	ctg	acc	tgc	acc	gtg	tct	ggc	tac	tca	att	144
Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Tyr	Ser	Ile	
		35					40					45				

acc	agc	gat	cat	gcc	tgg	agc	tgg	gtt	cgc	cag	cca	cct	gga	cga	ggg	192
Thr	Ser	Asp	His	Ala	Trp	Ser	Trp	Val	Arg	Gln	Pro	Pro	Gly	Arg	Gly	
	50					55				60						

ctt	gag	tgg	att	gga	tac	att	agt	tat	agt	gga	atc	aca	acc	tat	aat	240
Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Ser	Tyr	Ser	Gly	Ile	Thr	Thr	Tyr	Asn	
65				70						75				80		

cca	tct	ctc	aaa	tcc	aga	gtg	aca	atg	ctg	aga	gac	acc	agc	aag	aac	288
Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Met	Leu	Arg	Asp	Thr	Ser	Lys	Asn	
			85					90						95		

cag	ttc	agc	ctg	aga	ctc	agc	agc	gtg	aca	gcc	gcc	gac	acc	gcg	gtt	336
Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	
			100					105					110			

tat	tat	tgt	gca	aga	tcc	cta	gct	cgg	act	acg	gct	atg	gac	tac	tgg	384
Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Ala	Arg	Thr	Thr	Ala	Met	Asp	Tyr	Trp	
		115				120						125				

ggg	caa	ggc	agc	ctc	gtc	aca	gtc	tcc	tca	ggg	ggg	ggg	ggg	tcg	ggg	432
Gly	Gln	Gly	Ser	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
	130					135						140				

ggt ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg acc cag agc 480  
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser 160  
 145 150 155

cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt 528  
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys 175  
 165 170

aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag 576  
 Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys 190  
 180 185

cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac 624  
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His 205  
 195 200

tct ggt gtg cca agc aga ttc agc ggt agc ggt acc gac ttc 672  
 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe 220  
 210 215

acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac 720  
 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr 240  
 225 230 235

tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag 768  
 Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys 255  
 245 250

gtg gaa atc aaa ggt ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt 816  
 Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly 270  
 260 265

ggc gga tgc gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt 864  
 Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly 285  
 275 280

ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc 912  
 Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly 300  
 290 295

tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct 960  
 Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro 320  
 305 310 315

gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca 1008  
 Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr 335  
 325 330

acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc 1056  
 Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr 350  
 340 345

agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac 1104  
 Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp 365  
 355 360

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
370 375 380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
385 390 395 400	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg	1248
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met	
405 410 415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
420 425 430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
435 440 445	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	1392
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
450 455 460	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	1440
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
465 470 475 480	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	1488
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
485 490 495	
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa	1536
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
500 505 510	
ggg acc aag gtg gaa atc aaa gtg gcc ctg cac agg ccc gat gtc tac	1584
Gly Thr Lys Val Glu Ile Lys Val Ala Leu His Arg Pro Asp Val Tyr	
515 520 525	
ttg ctg cca cca gcc cgg gag cag ctg aac ctg cgc gag tcg gcc acc	1632
Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr	
530 535 540	
atc acg tgc ctg gtg acg ggc ttc tct ccc gcg gac gtc ttc gtg cag	1680
Ile Thr Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln	
545 550 555 560	
tgg atg cag agg ggg cag ccc ttg tcc ccg gag aag tat gtg acc agc	1728
Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser	
565 570 575	
gcc cca atg cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc	1776
Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser	
580 585 590	
atc ctg acc gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc	1824



Ile Leu Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr  
595 600 605

tgc	gtg	gcc	cat	gag	gcc	ctg	ccc	aac	agg	gtc	acc	gag	agg	acc	gtg	1872
Cys	Val	Ala	His	Glu	Ala	Leu	Pro	Asn	Arg	Val	Thr	Glu	Arg	Thr	Val	
	610					615					620					

gag aag tcc acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag 1920  
Asp Lys Ser Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu  
625 630 635 640